

OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 22:57:24 ; Search time 4550.28 Seconds
(without alignments)
9527.774 Million cell updates/sec

Title: US-10-670-863-2_COPY_213_1274
Perfect score: 1062
Sequence: 1 atgacagcaaagcctctaag.....tccggttatgggttctgtaag 1062

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA Main:*

- 1: /cgn2_6/ptodata/1/pna/PCTUS1_COMB.seq:*
- 2: /cgn2_6/ptodata/1/pna/PCTUS2_COMB.seq:*
- 3: /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq:*
- 4: /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
- 5: /cgn2_6/ptodata/1/pna/US07_COMB.seq:*
- 6: /cgn2_6/ptodata/1/pna/US080_COMB.seq:*
- 7: /cgn2_6/ptodata/1/pna/US081_COMB.seq:*
- 8: /cgn2_6/ptodata/1/pna/US082_COMB.seq:*
- 9: /cgn2_6/ptodata/1/pna/US083_COMB.seq:*
- 10: /cgn2_6/ptodata/1/pna/US084_COMB.seq:*
- 11: /cgn2_6/ptodata/1/pna/US085_COMB.seq:*
- 12: /cgn2_6/ptodata/1/pna/US086_COMB.seq:*
- 13: /cgn2_6/ptodata/1/pna/US087_COMB.seq:*
- 14: /cgn2_6/ptodata/1/pna/US088_COMB.seq:*
- 15: /cgn2_6/ptodata/1/pna/US089_COMB.seq:*
- 16: /cgn2_6/ptodata/1/pna/US090_COMB.seq:*
- 17: /cgn2_6/ptodata/1/pna/US091_COMB.seq:*
- 18: /cgn2_6/ptodata/1/pna/US092A_COMB.seq:*
- 19: /cgn2_6/ptodata/1/pna/US092B_COMB.seq:*
- 20: /cgn2_6/ptodata/1/pna/US093A_COMB.seq:*
- 21: /cgn2_6/ptodata/1/pna/US093B_COMB.seq:*
- 22: /cgn2_6/ptodata/1/pna/US094_COMB.seq:*
- 23: /cgn2_6/ptodata/1/pna/US095A_COMB.seq:*
- 24: /cgn2_6/ptodata/1/pna/US095B_COMB.seq:*
- 25: /cgn2_6/ptodata/1/pna/US095C_COMB.seq:*
- 26: /cgn2_6/ptodata/1/pna/US095D_COMB.seq:*
- 27: /cgn2_6/ptodata/1/pna/US096A_COMB.seq:*
- 28: /cgn2_6/ptodata/1/pna/US096B_COMB.seq:*
- 29: /cgn2_6/ptodata/1/pna/US096C_COMB.seq:*
- 30: /cgn2_6/ptodata/1/pna/US096D_COMB.seq:*
- 31: /cgn2_6/ptodata/1/pna/US096E_COMB.seq:*
- 32: /cgn2_6/ptodata/1/pna/US097A_COMB.seq:*
- 33: /cgn2_6/ptodata/1/pna/US097B_COMB.seq:*
- 34: /cgn2_6/ptodata/1/pna/US097C_COMB.seq:*
- 35: /cgn2_6/ptodata/1/pna/US098A_COMB.seq:*
- 36: /cgn2_6/ptodata/1/pna/US098B_COMB.seq:*
- 37: /cgn2_6/ptodata/1/pna/US098C_COMB.seq:*
- 38: /cgn2_6/ptodata/1/pna/US098D_COMB.seq:*

39: /cgn2_6/ptodata/1/pna/US099A_COMB.seq: *
40: /cgn2_6/ptodata/1/pna/US099B_COMB.seq: *
41: /cgn2_6/ptodata/1/pna/US099C_COMB.seq: *
42: /cgn2_6/ptodata/1/pna/US099D_COMB.seq: *
43: /cgn2_6/ptodata/1/pna/US099E_COMB.seq: *
44: /cgn2_6/ptodata/1/pna/US099F_COMB.seq: *
45: /cgn2_6/ptodata/1/pna/US099G_COMB.seq: *
46: /cgn2_6/ptodata/1/pna/US100A_COMB.seq: *
47: /cgn2_6/ptodata/1/pna/US100B_COMB.seq: *
48: /cgn2_6/ptodata/1/pna/US101A_COMB.seq: *
49: /cgn2_6/ptodata/1/pna/US101B_COMB.seq: *
50: /cgn2_6/ptodata/1/pna/US102A_COMB.seq: *
51: /cgn2_6/ptodata/1/pna/US102B_COMB.seq: *
52: /cgn2_6/ptodata/1/pna/US103A_COMB.seq: *
53: /cgn2_6/ptodata/1/pna/US103B_COMB.seq: *
54: /cgn2_6/ptodata/1/pna/US104A_COMB.seq: *
55: /cgn2_6/ptodata/1/pna/US104B_COMB.seq: *
56: /cgn2_6/ptodata/1/pna/US105A_COMB.seq: *
57: /cgn2_6/ptodata/1/pna/US105B_COMB.seq: *
58: /cgn2_6/ptodata/1/pna/US106A_COMB.seq: *
59: /cgn2_6/ptodata/1/pna/US107A_COMB.seq: *
60: /cgn2_6/ptodata/1/pna/US107B_COMB.seq: *
61: /cgn2_6/ptodata/1/pna/US107C_COMB.seq: *
62: /cgn2_6/ptodata/1/pna/US107D_COMB.seq: *
63: /cgn2_6/ptodata/1/pna/US108A_COMB.seq: *
64: /cgn2_6/ptodata/1/pna/US108B_COMB.seq: *
65: /cgn2_6/ptodata/1/pna/US109A_COMB.seq: *
66: /cgn2_6/ptodata/1/pna/US109B_COMB.seq: *
67: /cgn2_6/ptodata/1/pna/US109C_COMB.seq: *
68: /cgn2_6/ptodata/1/pna/US110_COMB.seq: *
69: /cgn2_6/ptodata/1/pna/US6000_COMB.seq: *
70: /cgn2_6/ptodata/1/pna/US6001_COMB.seq: *
71: /cgn2_6/ptodata/1/pna/US6002_COMB.seq: *
72: /cgn2_6/ptodata/1/pna/US6003_COMB.seq: *
73: /cgn2_6/ptodata/1/pna/US6004_COMB.seq: *
74: /cgn2_6/ptodata/1/pna/US6005_COMB.seq: *
75: /cgn2_6/ptodata/1/pna/US6006_COMB.seq: *
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88: /cgn2_6/ptodata/1/pna/US6019_COMB.seq: *
89: /cgn2_6/ptodata/1/pna/US6020_COMB.seq: *
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91: /cgn2_6/ptodata/1/pna/US6022_COMB.seq: *
92: /cgn2_6/ptodata/1/pna/US6023A_COMB.seq: *
93: /cgn2_6/ptodata/1/pna/US6023B_COMB.seq: *
94: /cgn2_6/ptodata/1/pna/US6024_COMB.seq: *
95: /cgn2_6/ptodata/1/pna/US6025_COMB.seq: *
96: /cgn2_6/ptodata/1/pna/US6026_COMB.seq: *
97: /cgn2_6/ptodata/1/pna/US6027_COMB.seq: *
98: /cgn2_6/ptodata/1/pna/US6028_COMB.seq: *
99: /cgn2_6/ptodata/1/pna/US6029_COMB.seq: *
100: /cgn2_6/ptodata/1/pna/US6030_COMB.seq: *
101: /cgn2_6/ptodata/1/pna/US6031_COMB.seq: *
102: /cgn2_6/ptodata/1/pna/US6032_COMB.seq: *
103: /cgn2_6/ptodata/1/pna/US6033_COMB.seq: *
104: /cgn2_6/ptodata/1/pna/US6034_COMB.seq: *
105: /cgn2_6/ptodata/1/pna/US6035_COMB.seq: *

106: /cgn2_6/ptodata/1/pna/US6036_COMB.seq:*
 107: /cgn2_6/ptodata/1/pna/US6037_COMB.seq:*
 108: /cgn2_6/ptodata/1/pna/US6038_COMB.seq:*
 109: /cgn2_6/ptodata/1/pna/US6039_COMB.seq:*
 110: /cgn2_6/ptodata/1/pna/US6040_COMB.seq:*
 111: /cgn2_6/ptodata/1/pna/US6041_COMB.seq:*
 112: /cgn2_6/ptodata/1/pna/US6042_COMB.seq:*
 113: /cgn2_6/ptodata/1/pna/US6043_COMB.seq:*
 114: /cgn2_6/ptodata/1/pna/US6044_COMB.seq:*
 115: /cgn2_6/ptodata/1/pna/US6045_COMB.seq:*
 116: /cgn2_6/ptodata/1/pna/US6046_COMB.seq:*
 117: /cgn2_6/ptodata/1/pna/US6047_COMB.seq:*
 118: /cgn2_6/ptodata/1/pna/US6048_COMB.seq:*
 119: /cgn2_6/ptodata/1/pna/US6049_COMB.seq:*
 120: /cgn2_6/ptodata/1/pna/US6050_COMB.seq:*
 121: /cgn2_6/ptodata/1/pna/US6051_COMB.seq:*
 122: /cgn2_6/ptodata/1/pna/US6052_COMB.seq:*
 123: /cgn2_6/ptodata/1/pna/US6053_COMB.seq:*
 124: /cgn2_6/ptodata/1/pna/US6054_COMB.seq:*
 125: /cgn2_6/ptodata/1/pna/US6055_COMB.seq:*
 126: /cgn2_6/ptodata/1/pna/US6056_COMB.seq:*
 127: /cgn2_6/ptodata/1/pna/US6057_COMB.seq:*
 128: /cgn2_6/ptodata/1/pna/US6058_COMB.seq:*
 129: /cgn2_6/ptodata/1/pna/US6059_COMB.seq:*

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 22:38:19 ; Search time 1620.48 Seconds
 (without alignments)
 8309.150 Million cell updates/sec

Title: US-10-670-863-2_COPY_213_1274
 Perfect score: 1062
 Sequence: 1 atgacagcaaagcctctaag.....tccggttatgggttctgtaag 1062

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 21945288 seqs, 6339366203 residues

Total number of hits satisfying chosen parameters: 43890576

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Pending_Patents_NA_New:*
 1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
 2: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq2:*
 3: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
 4: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
 5: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
 6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
 7: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq1:*
 8: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
 9: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq10:*
 10: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
 11: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq3:*
 12: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq4:*

13: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq5:*
14: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq6:*
15: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq7:*
16: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq8:*
17: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq9:*
18: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:*
19: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq2:*
20: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq3:*
21: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq4:*
22: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq5:*
23: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 22:22:19 ; Search time 177.454 Seconds
(without alignments)
9183.943 Million cell updates/sec

Title: US-10-670-863-2_COPY_279_1274
Perfect score: 996
Sequence: 1 acaccagaaatctcatgcag.....tccgttatgggttctgtaag 996

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

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OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 00:34:19 ; Search time 704.717 Seconds
(without alignments)
9161.687 Million cell updates/sec

Title: US-10-670-863-2_COPY_279_1274
Perfect score: 996
Sequence: 1 acaccagaaatctcatgcag.....tccgttatgggttctgtaag 996

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 22:57:24 ; Search time 4267.5 Seconds
(without alignments)
9527.774 Million cell updates/sec

Title: US-10-670-863-2_COPY_279_i274

Perfect score: 996

Sequence: 1 acaccagaaatctcatgcag.....tccggttatgggttctgtaag 996

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents_NA Main:*

1: /cgn2_6/ptodata/1/pna/PCTUS1_COMB.seq: *
2: /cgn2_6/ptodata/1/pna/PCTUS2_COMB.seq: *
3: /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq: *
4: /cgn2_6/ptodata/1/pna/US06_COMB.seq: *
5: /cgn2_6/ptodata/1/pna/US07_COMB.seq: *
6: /cgn2_6/ptodata/1/pna/US080_COMB.seq: *
7: /cgn2_6/ptodata/1/pna/US081_COMB.seq: *
8: /cgn2_6/ptodata/1/pna/US082_COMB.seq: *
9: /cgn2_6/ptodata/1/pna/US083_COMB.seq: *
10: /cgn2_6/ptodata/1/pna/US084_COMB.seq: *
11: /cgn2_6/ptodata/1/pna/US085_COMB.seq: *
12: /cgn2_6/ptodata/1/pna/US086_COMB.seq: *
13: /cgn2_6/ptodata/1/pna/US087_COMB.seq: *
14: /cgn2_6/ptodata/1/pna/US088_COMB.seq: *
15: /cgn2_6/ptodata/1/pna/US089_COMB.seq: *
16: /cgn2_6/ptodata/1/pna/US090_COMB.seq: *
17: /cgn2_6/ptodata/1/pna/US091_COMB.seq: *
18: /cgn2_6/ptodata/1/pna/US092A_COMB.seq: *
19: /cgn2_6/ptodata/1/pna/US092B_COMB.seq: *
20: /cgn2_6/ptodata/1/pna/US093A_COMB.seq: *
21: /cgn2_6/ptodata/1/pna/US093B_COMB.seq: *
22: /cgn2_6/ptodata/1/pna/US094_COMB.seq: *
23: /cgn2_6/ptodata/1/pna/US095A_COMB.seq: *
24: /cgn2_6/ptodata/1/pna/US095B_COMB.seq: *
25: /cgn2_6/ptodata/1/pna/US095C_COMB.seq: *
26: /cgn2_6/ptodata/1/pna/US095D_COMB.seq: *
27: /cgn2_6/ptodata/1/pna/US096A_COMB.seq: *
28: /cgn2_6/ptodata/1/pna/US096B_COMB.seq: *
29: /cgn2_6/ptodata/1/pna/US096C_COMB.seq: *
30: /cgn2_6/ptodata/1/pna/US096D_COMB.seq: *
31: /cgn2_6/ptodata/1/pna/US096E_COMB.seq: *
32: /cgn2_6/ptodata/1/pna/US097A_COMB.seq: *
33: /cgn2_6/ptodata/1/pna/US097B_COMB.seq: *
34: /cgn2_6/ptodata/1/pna/US097C_COMB.seq: *
35: /cgn2_6/ptodata/1/pna/US098A_COMB.seq: *
36: /cgn2_6/ptodata/1/pna/US098B_COMB.seq: *
37: /cgn2_6/ptodata/1/pna/US098C_COMB.seq: *
38: /cgn2_6/ptodata/1/pna/US098D_COMB.seq: *
39: /cgn2_6/ptodata/1/pna/US099A_COMB.seq: *
40: /cgn2_6/ptodata/1/pna/US099B_COMB.seq: *
41: /cgn2_6/ptodata/1/pna/US099C_COMB.seq: *
42: /cgn2_6/ptodata/1/pna/US099D_COMB.seq: *
43: /cgn2_6/ptodata/1/pna/US099E_COMB.seq: *
44: /cgn2_6/ptodata/1/pna/US099F_COMB.seq: *
45: /cgn2_6/ptodata/1/pna/US099G_COMB.seq: *
46: /cgn2_6/ptodata/1/pna/US100A_COMB.seq: *
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Scoring table: IDENTITY_NUC
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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RESULT 1

US-09-574-942-2

; Sequence 2, Application US/09574942
 ; Patent No. 6358723
 ; GENERAL INFORMATION:
 ; APPLICANT: Eastman, Alan R.
 ; APPLICANT: Krieser, Ronald J.
 ; TITLE OF INVENTION: DEOXYRIBONUCLEASE II BETA PROTEINS AND cDNAS
 ; FILE REFERENCE: DC-0137
 ; CURRENT APPLICATION NUMBER: US/09/574,942
 ; CURRENT FILING DATE: 2000-05-19
 ; PRIOR APPLICATION NUMBER: 09/541,840
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 354
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 US-09-574-942-2

Query Match 100.0%; Score 1927; DB 3; Length 354;
 Best Local Similarity 100.0%; Pred. No. 1.6e-205;
 Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Db | 1 | MTAKPLRTVLSLLFFALSGVLGTPEISCRNEYGEAVDWFIFYKLPKRTSKASEEAGLQYL | 60 |
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| | | | |
| Db | 61 | YLDSTRQTNKSLYLINSTRSALGRTLQHLTDHNSNDTAYLIYNDGVPGSVNYSRQYG | 120 |
| Qy | 121 | HAKGLLVNRTQGFWLIHSPVKFPPVHGYEYPTSGRRYGQTGICITFGYSQFEEIDFQLL | 180 |
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| Db | 121 | HAKGLLVNRTQGFWLIHSPVKFPPVHGYEYPTSGRRYGQTGICITFGYSQFEEIDFQLL | 180 |
| Qy | 181 | VLQPNIIYSCFIPSTFHWKLIYMPRMCANSSSLKIPVRYLAELHSAQGLNFVHFAKSSFYT | 240 |
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| Db | 181 | VLQPNIIYSCFIPSTFHWKLIYMPRMCANSSSLKIPVRYLAELHSAQGLNFVHFAKSSFYT | 240 |
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RESULT 2

US-09-807-784B-1

; Sequence 1, Application US/09807784B
 ; Patent No. 6653118
 ; GENERAL INFORMATION:
 ; APPLICANT: Tanuma, Sei-ichi
 ; APPLICANT: Shiokawa, Daisuke
 ; TITLE OF INVENTION: No. 6653118e1 Deoxyribonuclease, Gene Encoding Thereof and Use Thereof
 ; FILE REFERENCE: 210792
 ; CURRENT APPLICATION NUMBER: US/09/807,784B
 ; CURRENT FILING DATE: 1999-08-17
 ; PRIOR APPLICATION NUMBER: JP 11-230870
 ; PRIOR FILING DATE: 1999-08-17
 ; NUMBER OF SEQ ID NOS: 15

; SEQ ID NO 1
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-807-784B-1

Query Match 100.0%; Score 1927; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.6e-205;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 YLDSTRQTNKSLYLYINSTRSALGRTLQHLTDHNSNDTAYLIYNDGVPGSVNYSRQYG 120
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Qy    241 DDIFTGWIAQKLKTHLLAQTWQKKKQELPSNCSLPYHVYNIKSIGVTSKSYFSSRQDHSK 300
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RESULT 3

US-09-949-434-2

; Sequence 2, Application US/09949434
; Patent No. 6767997
; GENERAL INFORMATION:
; APPLICANT: Eastman, Alan R.
; APPLICANT: Krieser, Ronald J.
; TITLE OF INVENTION: DEOXYRIBONUCLEASE II BETA PROTEINS AND cDNAS
; FILE REFERENCE: DC-0137
; CURRENT APPLICATION NUMBER: US/09/949,434
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/574,942
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Mus sp.

US-09-949-434-2

Query Match 100.0%; Score 1927; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.6e-205;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 YLDSTRQTNKSLYLYINSTRSALGRTLQHLTDHNSNDTAYLIYNDGVPGSVNYSRQYG 120
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Db     61 YLDSTRQTNKSLYLYINSTRSALGRTLQHLTDHNSNDTAYLIYNDGVPGSVNYSRQYG 120
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| Db | 121 | HAKGLLVWNR | TQGF | LIHS | VPKF | PPVH | GYEY | PTSG | RRYG | QTGI | CITF | GYSQ | FEEI | DFQL | 180 |
| | | | | | | | | | | | | | | | |
| Qy | 181 | VLQPN | IYSC | FI | PSTF | HWKL | IYMP | RCAN | SSSL | KIPV | RYLA | ELHS | AQGL | NFVH | FAKSSFYT 240 |
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| Db | 181 | VLQPN | IYSC | FI | PSTF | HWKL | IYMP | RCAN | SSSL | KIPV | RYLA | ELHS | AQGL | NFVH | FAKSSFYT 240 |
| | | | | | | | | | | | | | | | |
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| Db | 241 | DDIFT | GWIA | QKLK | THLL | AQTW | QKKK | QELP | SNCS | LPYH | VYNI | KSIG | VTSK | SYFS | SRQDHSK 300 |
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| Db | 301 | WCVSI | KGSAN | RWTC | IGDL | NRSL | HQAL | RGGG | FICT | KNHY | IYQA | FKLY | LRYG | FCK 354 | |

RESULT 2

US-09-541-840-2

; Sequence 2, Application US/09541840

; GENERAL INFORMATION:

; APPLICANT: Eastman, Alan R.

; APPLICANT: Krieser, Ronald J.

; TITLE OF INVENTION: DEOXYRIBONUCLEASE II BETA PROTEINS AND cDNAS

; FILE REFERENCE: DC-0125

; CURRENT APPLICATION NUMBER: US/09/541,840

; CURRENT FILING DATE: 2000-04-03

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 354

; TYPE: PRT

; ORGANISM: Mus sp.

US-09-541-840-2

Query Match 100.0%; Score 1927; DB 19; Length 354;
 Best Local Similarity 100.0%; Pred. No. 2.7e-193;
 Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| | | | | | | | | | | | | | | | |
| Db | 1 | MTAKPL | RTVL | SLLF | ALSG | VLGT | PEIS | CRNEY | GEAV | DFIF | YKLP | KRTS | KASE | EAGL | QYL 60 |
| | | | | | | | | | | | | | | | |
| Qy | 61 | YLDSTR | QTNK | SLYL | INSTR | SALGR | TLQH | LYDTH | NSTND | TAYLI | YNDG | VPGS | VNYS | RQYG 120 | |
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| Db | 61 | YLDSTR | QTNK | SLYL | INSTR | SALGR | TLQH | LYDTH | NSTND | TAYLI | YNDG | VPGS | VNYS | RQYG 120 | |
| | | | | | | | | | | | | | | | |
| Qy | 121 | HAKGLLVWNR | TQGF | LIHS | VPKF | PPVH | GYEY | PTSG | RRYG | QTGI | CITF | GYSQ | FEEI | DFQL | 180 |
| | | | | | | | | | | | | | | | |
| Db | 121 | HAKGLLVWNR | TQGF | LIHS | VPKF | PPVH | GYEY | PTSG | RRYG | QTGI | CITF | GYSQ | FEEI | DFQL | 180 |
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| Qy | 181 | VLQPN | IYSC | FI | PSTF | HWKL | IYMP | RCAN | SSSL | KIPV | RYLA | ELHS | AQGL | NFVH | FAKSSFYT 240 |
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| Qy | 241 | DDIFT | GWIA | QKLK | THLL | AQTW | QKKK | QELP | SNCS | LPYH | VYNI | KSIG | VTSK | SYFS | SRQDHSK 300 |
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RESULT 2

US-09-541-840-2

; Sequence 2, Application US/09541840

; GENERAL INFORMATION:

; APPLICANT: Eastman, Alan R.

; APPLICANT: Krieser, Ronald J.

; TITLE OF INVENTION: DEOXYRIBONUCLEASE II BETA PROTEINS AND cDNAS

; FILE REFERENCE: DC-0125

; CURRENT APPLICATION NUMBER: US/09/541,840

; CURRENT FILING DATE: 2000-04-03

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 354

; TYPE: PRT

; ORGANISM: Mus sp.

US-09-541-840-2

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 Best Local Similarity 100.0%; Pred. No. 4.3e-173;
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| Db | 1 | MTAKPLR | TVLSLLFFALSGVLGTPEISCRNEYGEAVDWFIFYKL | PKRTSKASEEAGLQYL | 60 |
| Qy | 61 | YLDSTRQ | TWNKSLYLINSTRSALGRTLQHL | YDTHNSTNDTAYLIYNDGVP | GSVNYSRQYG 120 |
| | | | | | |
| Db | 61 | YLDSTRQ | TWNKSLYLINSTRSALGRTLQHL | YDTHNSTNDTAYLIYNDGVP | GSVNYSRQYG 120 |
| Qy | 121 | HAKGLLV | WNRTQGFWLIHSVPKFPPVHGYEYPTSGRRYGQTGICITFGYSQFEEIDFQLL | 180 | |
| | | | | | |
| Db | 121 | HAKGLLV | WNRTQGFWLIHSVPKFPPVHGYEYPTSGRRYGQTGICITFGYSQFEEIDFQLL | 180 | |
| Qy | 181 | VLQPN | IYSCFIPSTFWKLIYMPRMCANSSSLKIPVRYLAELHSAQGLNFVHFAKSSFYT | 240 | |
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| Db | 181 | VLQPN | IYSCFIPSTFWKLIYMPRMCANSSSLKIPVRYLAELHSAQGLNFVHFAKSSFYT | 240 | |
| Qy | 241 | DDIFTG | WIAQKLKTHLLAQTWQKKKQELPSNCSLPYHVYNIKSIGVTSKSYFSSRQDHSK | 300 | |
| | | | | | |
| Db | 241 | DDIFTG | WIAQKLKTHLLAQTWQKKKQELPSNCSLPYHVYNIKSIGVTSKSYFSSRQDHSK | 300 | |
| Qy | 301 | WCVSIK | GSANRWTCIG | 316 | |
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| Db | 301 | WCVSIK | GSANRWTCIG | 316 | |

Title: US-10-670-863-2

RESULT 3

AF128888

LOCUS AF128888 1654 bp mRNA linear ROD 06-DEC-1999

DEFINITION Mus musculus deoxyribonuclease DLAD mRNA, complete cds.

ACCESSION AF128888

VERSION AF128888.1 GI:6175549

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1654)

AUTHORS Shiokawa,D. and Tanuma,S.

TITLE DLAD, a novel mammalian divalent cation-independent endonuclease with homology to DNase II

JOURNAL Nucleic Acids Res. 27 (20), 4083-4089 (1999)

MEDLINE 99428663

PUBMED 10497274

REFERENCE 2 (bases 1 to 1654)

AUTHORS Shiokawa,D. and Tanuma,S.

TITLE Direct Submission

JOURNAL Submitted (16-FEB-1999) Biochemistry, Science Univ. of Tokyo, Shinjuku-ku Ichigaya Funagawara-machi 12, Tokyo 162-0826, Japan

FEATURES Location/Qualifiers

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ORIGIN

Query Match 100.0%; Score 1652; DB 10; Length 1654;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 ATCAGATGACATGGGACTCAGCCTCTTCTGTTTGTGCCCAAACAGTGAACAGCAAAAGTG 120

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Db 121 AACCGACCCGCAAGGGAGCCAACGCGGCCTGAGAAAGACCTGACACTCTGACTCCACAGT 180

Qy 181 CCCCTGCATGGAATGAAGGCCACAGATAGAAAATGACAGCAAAGCCTCTAAGAACAGTTC 240
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Db 181 CCCCTGCATGGAATGAAGGCCACAGATAGAAAATGACAGCAAAGCCTCTAAGAACAGTTC 240

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| | | | |
|----|------|--|------|
| Db | 241 | TTTCTTTGCTCTTCTTTGCCCTCTCTGGGGTCTCTGGGGACACCAGAAATCTCATGCAGAA | 300 |
| Qy | 301 | ATGAATATGGTGAAGCTGTGGACTGGTTTATCTTTTATAAGTTACCCAAAAGGACTAGCA | 360 |
| Db | 301 | ATGAATATGGTGAAGCTGTGGACTGGTTTATCTTTTATAAGTTACCCAAAAGGACTAGCA | 360 |
| Qy | 361 | AGGCAAGTGAAGAGGCGGGGCTGCAGTACCTGTACCTGGACTCCACAAGACAAACCTGGA | 420 |
| Db | 361 | AGGCAAGTGAAGAGGCGGGGCTGCAGTACCTGTACCTGGACTCCACAAGACAAACCTGGA | 420 |
| Qy | 421 | ACAAGAGCCTCTACCTGATTAAACAGCACCAGGAGTGCTCTGGGGAGGACCTTACAGCATC | 480 |
| Db | 421 | ACAAGAGCCTCTACCTGATTAAACAGCACCAGGAGTGCTCTGGGGAGGACCTTACAGCATC | 480 |
| Qy | 481 | TGTATGACACACATAATTCCACGAATGACACAGCCTATCTAATATACAACGATGGTGTCC | 540 |
| Db | 481 | TGTATGACACACATAATTCCACGAATGACACAGCCTATCTAATATACAACGATGGTGTCC | 540 |
| Qy | 541 | CTGGATCTGTGAATTACAGCAGACAGTATGGACATGCCAAAGGTCTGCTGGTATGGAACA | 600 |
| Db | 541 | CTGGATCTGTGAATTACAGCAGACAGTATGGACATGCCAAAGGTCTGCTGGTATGGAACA | 600 |
| Qy | 601 | GAACGCAGGGGTTCTGGCTGATACACTCTGTTCCCAAGTTTCCCCAGTTCATGGCTATG | 660 |
| Db | 601 | GAACGCAGGGGTTCTGGCTGATACACTCTGTTCCCAAGTTTCCCCAGTTCATGGCTATG | 660 |
| Qy | 661 | AGTACCCAACCTCGGGGAGGCGATATGGACAAACCGGCATCTGCATCACTTTCGGATACA | 720 |
| Db | 661 | AGTACCCAACCTCGGGGAGGCGATATGGACAAACCGGCATCTGCATCACTTTCGGATACA | 720 |
| Qy | 721 | GCCAGTTTGAGGAAATAGATTTTCAGCTCTTGGTCTTACAACCAAACATCTACAGCTGCT | 780 |
| Db | 721 | GCCAGTTTGAGGAAATAGATTTTCAGCTCTTGGTCTTACAACCAAACATCTACAGCTGCT | 780 |
| Qy | 781 | TCATTCCAAGCACCTTTCACTGGAACTTATCTACATGCCCCGGATGTGTGCCAACTCCA | 840 |
| Db | 781 | TCATTCCAAGCACCTTTCACTGGAACTTATCTACATGCCCCGGATGTGTGCCAACTCCA | 840 |
| Qy | 841 | GTTCCTTAAAGATCCCTGTCCGGTACCTCGCTGAACTGCACTCAGCCCAGGGTCTAAACT | 900 |
| Db | 841 | GTTCCTTAAAGATCCCTGTCCGGTACCTCGCTGAACTGCACTCAGCCCAGGGTCTAAACT | 900 |
| Qy | 901 | TCGTCCATTTTGCAAAATCAAGTTTTTATACTGATGACATCTTTACAGGATGGATAGCTC | 960 |
| Db | 901 | TCGTCCATTTTGCAAAATCAAGTTTTTATACTGATGACATCTTTACAGGATGGATAGCTC | 960 |
| Qy | 961 | AAAAGTTGAAGACACATTTGTTAGCACAAACCTGGCAGAAAAAGAAACAAGAGCTTCCTT | 1020 |
| Db | 961 | AAAAGTTGAAGACACATTTGTTAGCACAAACCTGGCAGAAAAAGAAACAAGAGCTTCCTT | 1020 |
| Qy | 1021 | CAAACGTTCCTGCCTTACCATGTCTACAACATCAAGTCCATTGGGGTAACTTCCAAGT | 1080 |
| Db | 1021 | CAAACGTTCCTGCCTTACCATGTCTACAACATCAAGTCCATTGGGGTAACTTCCAAGT | 1080 |
| Qy | 1081 | CTTACTTCAGTTCTCGCCAAGACCATTCCAAATGGTGTGTTTCCATAAAGGGCTCCGCAA | 1140 |
| Db | 1081 | CTTACTTCAGTTCTCGCCAAGACCATTCCAAATGGTGTGTTTCCATAAAGGGCTCCGCAA | 1140 |
| Qy | 1141 | ATCGCTGGACCTGCATTGGAGACCTAAATCGAAGCCTACACCAAGCCTTAAGAGGTGGAG | 1200 |
| Db | 1141 | ATCGCTGGACCTGCATTGGAGACCTAAATCGAAGCCTACACCAAGCCTTAAGAGGTGGAG | 1200 |
| Qy | 1201 | GATTCATCTGTACAAAGAATCACTACATTTACCAGGCATTTTCATAAAATTATATCTCCGTT | 1260 |
| Db | 1201 | GATTCATCTGTACAAAGAATCACTACATTTACCAGGCATTTTCATAAAATTATATCTCCGTT | 1260 |

| | | | |
|----|------|--|------|
| Qy | 1261 | ATGGGTTCTGTAAGTAAACTCGGTGAAAGGCCACACCCCTCTGTCCTTGAAAACTGGCA | 1320 |
| Db | 1261 | ATGGGTTCTGTAAGTAAACTCGGTGAAAGGCCACACCCCTCTGTCCTTGAAAACTGGCA | 1320 |
| Qy | 1321 | CTGGAACATCTCGCCTTGGATCTGTTCTCCATAATTTCAAGGCTTCTGAGTGAGCACAAC | 1380 |
| Db | 1321 | CTGGAACATCTCGCCTTGGATCTGTTCTCCATAATTTCAAGGCTTCTGAGTGAGCACAAC | 1380 |
| Qy | 1381 | GTAGCGTCCAATAAAAGCACTGTGAGCCACATTTACCTTCCTATGTTCAAATCAAGAGA | 1440 |
| Db | 1381 | GTAGCGTCCAATAAAAGCACTGTGAGCCACATTTACCTTCCTATGTTCAAATCAAGAGA | 1440 |
| Qy | 1441 | AATAGGAGTCATCTGCATGTATGGAATTAGAAATCAAAATCATGATATGTAAGTAATAGC | 1500 |
| Db | 1441 | AATAGGAGTCATCTGCATGTATGGAATTAGAAATCAAAATCATGATATGTAAGTAATAGC | 1500 |
| Qy | 1501 | ACCAGGGGACAGAATACAATATTTTCTCCAGTTTAATTACCTTCAGTGGTCTGTCTTGT | 1560 |
| Db | 1501 | ACCAGGGGACAGAATACAATATTTTCTCCAGTTTAATTACCTTCAGTGGTCTGTCTTGT | 1560 |
| Qy | 1561 | GGATTAAGTTTCATCTCTCACAAGCAACCCTGACTGTCCTGTTTGAAGAAATAAAGGTG | 1620 |
| Db | 1561 | GGATTAAGTTTCATCTCTCACAAGCAACCCTGACTGTCCTGTTTGAAGAAATAAAGGTG | 1620 |
| Qy | 1621 | CCCTCCTCCCCCTTAAAAAAAAAAAAAAAAAAAA | 1652 |
| Db | 1621 | CCCTCCTCCCCCTTAAAAAAAAAAAAAAAAAAAA | 1652 |

RESULT 7

AF178974

LOCUS AF178974 1498 bp mRNA linear ROD 29-NOV-1999

DEFINITION Rattus norvegicus deoxyribonuclease DLAD mRNA, complete cds.

ACCESSION AF178974

VERSION AF178974.1 GI:6470130

KEYWORDS

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 1498)

AUTHORS Tanuma,S. and Shiokawa,D.

TITLE Cloning of a cDNA encoding a rat DNase II-like acid DNase

JOURNAL Biochem. Biophys. Res. Commun. 265 (2), 395-399 (1999)

MEDLINE 20025354

PUBMED 10558878

REFERENCE 2 (bases 1 to 1498)

AUTHORS Shiokawa,D. and Tanuma,S.

TITLE Direct Submission

JOURNAL Submitted (19-AUG-1999) Biochemistry, Science University of Tokyo, Shinjuku-ku Ichigaya Funagawara-machi 12, Tokyo 162-0826, Japan

FEATURES

source Location/Qualifiers

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Db 846 CTAAACTTCCTCCATTTTTCGCGAAATCAACTTTTTTATACTGATGACATCTTTGTCAGCCTGG 905

Qy 954 ATAGCTCAAAAGTTGAAGACACATTTGTAGCACAAACCTGGCAGAAAAAGAAACAAGAG 1013
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Db 906 ATAGCTCAAAAGCTGAAGGTGCATTTGCTGGTAGAATCCTGGCAGCGAAAGAACCACGAG 965

Qy 1014 CTTCCCTTCAAACGTTCCTGCCTTACCATGTCTACAACATCAAGTCCATTGGGGTAACT 1073
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Db 1026 CTGCAGTCCGACTTCCCTTCTCATCACGACCATTCCAAATGGTGTGTTTCCACAAAGGAC 1085

Qy 1134 TCCGCAAATCGCTGGACCTGCATTGGAGACCTAAATCGAAGCCTACACCAAGCCTTAAGA 1193
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Db 1086 TCTCAGGCTCGCTGGACCTGTATTGGAGACCTAAATCGGAGCCACATCAAGCCTTGAGA 1145

Qy 1194 GGTGGAGGATTTCATCTGTACAAAGAATCACTACATTTACCAGGCATTTTATAAAATTATAT 1253
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Db 1146 AGTGGAGGATTTATCTGTTTGAAGAATCGGTACATTTACCAGTCATTTGATAGGTTAGTT 1205

Qy 1254 CTCCGTTATGGGTTCTGTAAGTAAACTCGGTGAAAGGCCACACCCTCTGTCTTGAAGAAC 1313
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Db 1206 TCCCATTATGCCTCCTGTAACTAAGCTTGGGGAAAGGTCCCACCCACTGCCCTTAAAGAC 1265

Qy 1314 ACTGGCACTGGAACATCTCGCCTTGGATCTGTTCTCCATAATTTCAAGGCTTCTGAGTGA 1373
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Db 1266 ACTGGCTCTGGGACATCTTGCCTTGGATCTATTTCTCCATATGTTAAAGGTTTCTGAGTG- 1324

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RESULT 2

US-09-574-942-1

; Sequence 1, Application US/09574942

; Patent No. 6358723

; GENERAL INFORMATION:

; APPLICANT: Eastman, Alan R.

; APPLICANT: Krieser, Ronald J.

; TITLE OF INVENTION: DEOXYRIBONUCLEASE II BETA PROTEINS AND cDNAS

; FILE REFERENCE: DC-0137

; CURRENT APPLICATION NUMBER: US/09/574,942

; CURRENT FILING DATE: 2000-05-19

; PRIOR APPLICATION NUMBER: 09/541,840

; PRIOR FILING DATE: 2000-04-03

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1224

; TYPE: DNA

; ORGANISM: Mus sp.

US-09-574-942-1



Query Match 73.8%; Score 1219.8; DB 3; Length 1224;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1221; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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| Qy | 235 | CAGTTCTTTCTTTGCTCTTCTTTGCCCTCTCTGGGGTCTCTGGGGACACCAGAAATCTCAT | 294 |
| Db | 62 | CAGTTCTTTCTTTGCTCTTCTTTGCCCTCTCTGGGGTCTCTGGGGACACCAGAAATCTCAT | 121 |
| Qy | 295 | GCAGAAATGAATATGGTGAAGCTGTGGAAGTGGTTTATCTTTTATAAGTTACCCAAAAGGA | 354 |
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| Qy | 415 | CCTGGAACAAGAGCCTCTACCTGATTAAACAGCACACAGGAGTGCTCTGGGGAGGACCTTAC | 474 |
| Db | 242 | CCTGGAACAAGAGCCTCTACCTGATTAAACAGCACACAGGAGTGCTCTGGGGAGGACCTTAC | 301 |
| Qy | 475 | AGCATCTGTATGACACACATAATTCCACGAATGACACAGCCTATCTAATATACAACGATG | 534 |
| Db | 302 | AGCATCTGTATGACACACATAATTCCACGAATGACACAGCCTATCTAATATACAACGATG | 361 |
| Qy | 535 | GTGTCCCTGGATCTGTGAATTACAGCAGACAGTATGGACATGCCAAAGGTCTGCTGGTAT | 594 |
| Db | 362 | GTGTCCCTGGATCTGTGAATTACAGCAGACAGTATGGACATGCCAAAGGTCTGCTGGTAT | 421 |
| Qy | 595 | GGAACAGAACGCAGGGGTTCTGGCTGATACACTCTGTTCCCAAGTTTCCCCAGTTCATG | 654 |
| Db | 422 | GGAACAGAACGCAGGGGTTCTGGCTGATACACTCTGTTCCCAAGTTTCCCCAGTTCATG | 481 |
| Qy | 655 | GCTATGAGTACCCAACCTCGGGGAGGCGATATGGACAAACCGGCATCTGCATCACTTTCG | 714 |
| Db | 482 | GCTATGAGTACCCAACCTCGGGGAGGCGATATGGACAAACCGGCATCTGCATCACTTTCG | 541 |
| Qy | 715 | GATACAGCCAGTTTGAGGAAATAGATTTTTCAGCTCTTGGTCTTACAACCAAACATCTACA | 774 |
| Db | 542 | GATACAGCCAGTTTGAGGAAATAGATTTTTCAGCTCTTGGTCTTACAACCAAACATCTACA | 601 |
| Qy | 775 | GCTGCTTCATTCCAAGCACCTTTCACTGGAACCTTATCTACATGCCCCGGATGTGTGCCA | 834 |
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| Qy | 835 | ACTCCAGTTCCTTAAAGATCCCTGTCCGGTACCTCGCTGAACTGCACTCAGCCCAGGGTC | 894 |
| Db | 662 | ACTCCAGTTCCTTAAAGATCCCTGTCCGGTACCTCGCTGAACTGCACTCAGCCCAGGGTC | 721 |
| Qy | 895 | TAAACTTCGTCCATTTTGCAAAATCAAGTTTTTATACTGATGACATCTTTACAGGATGGA | 954 |
| Db | 722 | TAAACTTCGTCCATTTTGCAAAATCAAGTTTTTATACTGATGACATCTTTACAGGATGGA | 781 |
| Qy | 955 | TAGCTCAAAAGTTGAAGACACATTTGTTAGCACAAACCTGGCAGAAAAAGAAACAAGAGC | 1014 |
| Db | 782 | TAGCTCAAAAGTTGAAGACACATTTGTTAGCACAAACCTGGCAGAAAAAGAAACAAGAGC | 841 |
| Qy | 1015 | TTCTTCAAACCTGTTCCCTGCCTTACCATGTCTACAACATCAAGTCCATTGGGGTAACTT | 1074 |
| Db | 842 | TTCTTCAAACCTGTTCCCTGCCTTACCATGTCTACAACATCAAGTCCATTGGGGTAACTT | 901 |
| Qy | 1075 | CCAAGTCTTACTTCAGTTCTCGCCAAGACCATTCCAAATGGTGTGTTTCCATAAAGGGCT | 1134 |
| Db | 902 | CCAAGTCTTACTTCAGTTCTCGCCAAGACCATTCCAAATGGTGTGTTTCCATAAAGGGCT | 961 |
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Db      1022 GTGGAGGATTTCATCTGTACAAAGAATCACTACATTTACCAGGCATTTTCATAAAATTATATC 1081
Qy      1255 TCCGTTTATGGGTTCTGTAAAGTAAACTCGGTGAAAGGCCACACCCTCTGTCCTTGAAAACA 1314
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Db      1082 TCCGTTTATGGGTTCTGTAAAGTAAACTCGGTGAAAGGCCACACCCTCTGTCCTTGAAAACA 1141
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Db      1142 CTGGCACTGGAACATCTCGCCTTGGATCTGTTCTCCATAATATCAAGGCTTCTGAGTGAG 1201
Qy      1375 CACAACGTAGCGTCCAATAAAAAG 1397
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Db      1202 CACAACGTAGCGTCCAATAAAAAG 1224

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RESULT 3

US-09-949-434-1

; Sequence 1, Application US/09949434

; Patent No. 6767997

; GENERAL INFORMATION:

; APPLICANT: Eastman, Alan R.

; APPLICANT: Krieser, Ronald J.

; TITLE OF INVENTION: DEOXYRIBONUCLEASE II BETA PROTEINS AND cDNAS

; FILE REFERENCE: DC-0137

; CURRENT APPLICATION NUMBER: US/09/949,434

; CURRENT FILING DATE: 2001-09-07

; PRIOR APPLICATION NUMBER: 09/574,942

; PRIOR FILING DATE: 2000-05-19

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1224

; TYPE: DNA

; ORGANISM: Mus sp.

US-09-949-434-1

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Query Match          73.8%;  Score 1219.8;  DB 4;  Length 1224;
Best Local Similarity 99.8%;  Pred. No. 0;
Matches 1221;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db      122 GCAGAAATGAATATGGTGAAGCTGTGGACTGGTTTATCTTTTATAAGTTACCCAAAAGGA 181
Qy      355 CTAGCAAGGCAAGTGAAGAGGCGGGGCTGCAGTACCTGTACCTGGACTCCACAAGACAAA 414
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Db      182 CTAGCAAGGCAAGTGAAGAGGCGGGGCTGCAGTACCTGTACCTGGACTCCACAAGACAAA 241
Qy      415 CCTGGAACAAGAGCCTCTACCTGATTAACAGCACCAGGAGTGCTCTGGGGAGGACCTTAC 474
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Db      242 CCTGGAACAAGAGCCTCTACCTGATTAACAGCACCAGGAGTGCTCTGGGGAGGACCTTAC 301
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        |||
Db      302 AGCATCTGTATGACACACATAATTCCACGAATGACACAGCCTATCTAATATACAACGATG 361

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| | | | |
|----|------|---|------|
| Qy | 535 | GTGTCCCTGGATCTGTGAATTACAGCAGACAGTATGGACATGCCAAAGGTCTGCTGGTAT | 594 |
| | | | |
| Db | 362 | GTGTCCCTGGATCTGTGAATTACAGCAGACAGTATGGACATGCCAAAGGTCTGCTGGTAT | 421 |
| Qy | 595 | GGAACAGAACGCAGGGGTTCTGGCTGATACACTCTGTTCCCAAGTTTCCCCCAGTTCATG | 654 |
| | | | |
| Db | 422 | GGAACAGAACGCAGGGGTTCTGGCTGATACACTCTGTTCCCAAGTTTCCCCCAGTTCATG | 481 |
| Qy | 655 | GCTATGAGTACCCAACCTCGGGGAGGCGATATGGACAAACCGGCATCTGCATCACTTTTCG | 714 |
| | | | |
| Db | 482 | GCTATGAGTACCCAACCTCGGGGAGGCGATATGGACAAACCGGCATCTGCATCACTTTTCG | 541 |
| Qy | 715 | GATACAGCCAGTTTGTAGGAAATAGATTTTCAGCTCTTGGTCTTACAACCAAACATCTACA | 774 |
| | | | |
| Db | 542 | GATACAGCCAGTTTGTAGGAAATAGATTTTCAGCTCTTGGTCTTACAACCAAACATCTACA | 601 |
| Qy | 775 | GCTGCTTCATTCCAAGCACCTTTCACCTGGAAACTTATCTACATGCCCCGGATGTGTGCCA | 834 |
| | | | |
| Db | 602 | GCTGCTTCATTCCAAGCACCTTTCACCTGGAAACTTATCTACATGCCCCGGATGTGTGCCA | 661 |
| Qy | 835 | ACTCCAGTTCCTTAAAGATCCCTGTCCGGTACCTCGCTGAACTGCACTCAGCCCAGGGTC | 894 |
| | | | |
| Db | 662 | ACTCCAGTTCCTTAAAGATCCCTGTCCGGTACCTCGCTGAACTGCACTCAGCCCAGGGTC | 721 |
| Qy | 895 | TAAACTTCGTCCATTTTGCAAAATCAAGTTTTTATACTGATGACATCTTTACAGGATGGA | 954 |
| | | | |
| Db | 722 | TAAACTTCGTCCATTTTGCAAAATCAAGTTTTTATACTGATGACATCTTTACAGGATGGA | 781 |
| Qy | 955 | TAGCTCAAAAGTTGAAGACACATTTGTTAGCACAAACCTGGCAGAAAAAGAAACAAGAGC | 1014 |
| | | | |
| Db | 782 | TAGCTCAAAAGTTGAAGACACATTTGTTAGCACAAACCTGGCAGAAAAAGAAACAAGAGC | 841 |
| Qy | 1015 | TTCTTCAAACCTGTTCCCTGCCTTACCATGTCTACAACATCAAGTCCATTGGGGTAACTT | 1074 |
| | | | |
| Db | 842 | TTCTTCAAACCTGTTCCCTGCCTTACCATGTCTACAACATCAAGTCCATTGGGGTAACTT | 901 |
| Qy | 1075 | CCAAGTCTTACTTCAGTTCTCGCCAAGACCATTCCAAATGGTGTGTTTCCATAAAGGGCT | 1134 |
| | | | |
| Db | 902 | CCAAGTCTTACTTCAGTTCTCGCCAAGACCATTCCAAATGGTGTGTTTCCATAAAGGGCT | 961 |
| Qy | 1135 | CCGCAAATCGCTGGACCTGCATTGGAGACCTAAATCGAAGCCTACACCAAGCCTTAAGAG | 1194 |
| | | | |
| Db | 962 | CCGCAAATCGCTGGACCTGCATTGGAGACCTAAATCGAAGCCTACACCAAGCCTTAAGAG | 1021 |
| Qy | 1195 | GTGGAGGATTCATCTGTACAAAGAATCACTACATTTACCAGGCATTTTCATAAATTATATC | 1254 |
| | | | |
| Db | 1022 | GTGGAGGATTCATCTGTACAAAGAATCACTACATTTACCAGGCATTTTCATAAATTATATC | 1081 |
| Qy | 1255 | TCCGTTATGGGTTCTGTAAGTAAACTCGGTGAAAGGCCACACCCTCTGTCCTTGAAAACA | 1314 |
| | | | |
| Db | 1082 | TCCGTTATGGGTTCTGTAAGTAAACTCGGTGAAAGGCCACACCCTCTGTCCTTGAAAACA | 1141 |
| Qy | 1315 | CTGGCACTGGAACATCTCGCCTTGGATCTGTTCTCCATAATTTCAAGGCTTCTGAGTGAG | 1374 |
| | | | |
| Db | 1142 | CTGGCACTGGAACATCTCGCCTTGGATCTGTTCTCCATAATATCAAGGCTTCTGAGTGAG | 1201 |
| Qy | 1375 | CACAACGTAGCGTCCAATAAAAAG | 1397 |
| | | | |
| Db | 1202 | CACAACGTAGCGTCCAATAAAAAG | 1224 |

RESULT 4

US-09-574-942-3

; Sequence 3, Application US/09574942

; Patent No. 6358723

; GENERAL INFORMATION:

; APPLICANT: Eastman, Alan R.
 ; APPLICANT: Krieser, Ronald J.
 ; TITLE OF INVENTION: DEOXYRIBONUCLEASE II BETA PROTEINS AND cDNAS
 ; FILE REFERENCE: DC-0137
 ; CURRENT APPLICATION NUMBER: US/09/574,942
 ; CURRENT FILING DATE: 2000-05-19
 ; PRIOR APPLICATION NUMBER: 09/541,840
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 1268
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-574-942-3

Query Match 40.8%; Score 673.8; DB 3; Length 1268;
 Best Local Similarity 75.1%; Pred. No. 4.3e-208;
 Matches 884; Conservative 0; Mismatches 282; Indels 11; Gaps 3;

| | | | |
|----|-----|---|-----|
| Qy | 204 | AGATAGAAAATGACAGCAAAGCCTCTAAGAACAGTTCTTTCTTTGCTCTTCTTTGCCCTC | 263 |
| | | | |
| Db | 37 | AAACAGAAAATGATGGCAAGACTGCTAAGAACATCCTTTGCTTTGCTCTTCCTTGGCCTC | 96 |
| Qy | 264 | TCTGGGGTCTGGGGACACCAGAAATCTCATGCAGAAATGAATATGGTGAAGCTGTGGAC | 323 |
| | | | |
| Db | 97 | TTTGGGGTGTCTGGGGGACAGCAACAATTTTCATGCAGAAATGAAGAAGGGAAAGCTGTGGAC | 156 |
| Qy | 324 | TGGTTTATCTTTTATAAGTTACCCAAAAGGACTAGCAAGGCAAGTGAAGAGGCGGGGCTG | 383 |
| | | | |
| Db | 157 | TGGTTTACTTTTATAAGTTACCTAAAAGACAAAACAAGGAAAGTGGAGAGACTGGGTTA | 216 |
| Qy | 384 | CAGTACCTGTACCTGGACTCCACAAGACAAACCTGGAACAAGAGCCTCTACCTGATTAAC | 443 |
| | | | |
| Db | 217 | GAGTACCTGTACCTAGACTCTACAAC TAGAAGCTGGAGGAAGAGTGAGCAACTAATGAAT | 276 |
| Qy | 444 | AGCACCAGGAGTGCTCTGGGGAGGACCTTACAGCATCTGTATGACACACATAATTCCACG | 503 |
| | | | |
| Db | 277 | GACACCAAGAGTGTTTTGGGAAGGACATTACAACAGCTATATGAAGCATATGCCTCTAAG | 336 |
| Qy | 504 | AAT---GACACAGCCTATCTAATATACAACGATGGTGTCCCTGGATCTGTGAATTACAGC | 560 |
| | | | |
| Db | 337 | AGTAACAACACAGCCTATCTAATATACAATGATGGAGTCCCTAAACCTGTGAATTACAGT | 396 |
| Qy | 561 | AGACAGTATGGACATGCCAAAGGTCTGCTGGTATGGAACAGAACGCAGGGGTTCTGGCTG | 620 |
| | | | |
| Db | 397 | AGAAAGTATGGACACACCAAAGGTTTACTGCTGTGGAACAGAGTTCAAGGGTTCTGGCTG | 456 |
| Qy | 621 | ATACACTCTGTTCCCAAGTTTCCCCCAGTTC-----ATGGCTATGAGTACCCAACCTCG | 674 |
| | | | |
| Db | 457 | ATTCAATCCATCCCTCAGTTTCCTCCAATTCCGGAAGAAGGCTATGATTATCCACCCACA | 516 |
| Qy | 675 | GGGAGGCGATATGGACAAACCGGCATCTGCATCACTTTTCGGATACAGCCAGTTTGAGGAA | 734 |
| | | | |
| Db | 517 | GGGAGACGAAATGGACAAAGTGGCATCTGCATAACTTTCAAGTACAACCAGTATGAGGCA | 576 |
| Qy | 735 | ATAGATTTTTCAGCTCTTGGTCTTACAACCAAACATCTACAGCTGCTTCATTCCAAGCACC | 794 |
| | | | |
| Db | 577 | ATAGATTCTCAGCTCTTGGTCTGCAACCCCAACGTCTATAGCTGCTCCATCCCAGCCACC | 636 |
| Qy | 795 | TTTCACTGGAAACTTATCTACATGCCCCGGATGTGTGCCAACTCCAGTTCCTTAAAGATC | 854 |
| | | | |
| Db | 637 | TTTCAACCAGGAGCTCATTCACATGCCCCAGCTGTGCACCAGGGCCAGCTCATCAGAGATT | 696 |
| Qy | 855 | CCTGTCCGGTACCTCGCTGAACTGCACTCAGCCCAGGGTCTAAACTTCGTCCATTTTGCA | 914 |
| | | | |
| Db | 697 | CCTGGCAGGCTCCTCACCACACTTCAGTCGGCCCAGGGACAAAAATTCCTCCATTTTGCA | 756 |

FEATURES
source Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="IMAGE:1450676"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."

ORIGIN

Query Match 32.9%; Score 543; DB 1; Length 543;
Best Local Similarity 100.0%; Pred. No. 4.9e-145;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|----|-----|---|-----|
| Qy | 16 | GCACAAAGGCTCCCAGAGTCACACTGGAATGTTGTGACAGAACCCATCAGATGACATGGG | 75 |
| Db | 1 | GCACAAAGGCTCCCAGAGTCACACTGGAATGTTGTGACAGAACCCATCAGATGACATGGG | 60 |
| Qy | 76 | ACTCAGCCTCTTCTGTTTGTGCCCAAACAGTGAACAGCAAAGTGAACCGACCCGCAAGG | 135 |
| Db | 61 | ACTCAGCCTCTTCTGTTTGTGCCCAAACAGTGAACAGCAAAGTGAACCGACCCGCAAGG | 120 |
| Qy | 136 | GAGCCAACGCGGCCTGAGAAAGACCTGACACTCTGACTCCACAGTCCCCTGCATGGAATG | 195 |
| Db | 121 | GAGCCAACGCGGCCTGAGAAAGACCTGACACTCTGACTCCACAGTCCCCTGCATGGAATG | 180 |
| Qy | 196 | AAGGCCACAGATAGAAAAATGACAGCAAAGCCTCTAAGAACAGTTCTTTCTTTGCTCTTCT | 255 |
| Db | 181 | AAGGCCACAGATAGAAAAATGACAGCAAAGCCTCTAAGAACAGTTCTTTCTTTGCTCTTCT | 240 |
| Qy | 256 | TTGCCCTCTCTGGGGTCCCTGGGGACACCAGAAATCTCATGCAGAAATGAATATGGTGAAG | 315 |
| Db | 241 | TTGCCCTCTCTGGGGTCCCTGGGGACACCAGAAATCTCATGCAGAAATGAATATGGTGAAG | 300 |
| Qy | 316 | CTGTGGACTGGTTTATCTTTTATAAGTTACCCAAAAGGACTAGCAAGGCAAGTGAAGAGG | 375 |
| Db | 301 | CTGTGGACTGGTTTATCTTTTATAAGTTACCCAAAAGGACTAGCAAGGCAAGTGAAGAGG | 360 |
| Qy | 376 | CGGGGCTGCAGTACCTGTACCTGGACTCCACAAGACAAACCTGGAACAAGAGCCTCTACC | 435 |
| Db | 361 | CGGGGCTGCAGTACCTGTACCTGGACTCCACAAGACAAACCTGGAACAAGAGCCTCTACC | 420 |
| Qy | 436 | TGATTAACAGCACCAGGAGTGCTCTGGGGAGGACCTTACAGCATCTGTATGACACACATA | 495 |
| Db | 421 | TGATTAACAGCACCAGGAGTGCTCTGGGGAGGACCTTACAGCATCTGTATGACACACATA | 480 |
| Qy | 496 | ATTCCACGAATGACACAGCCTATCTAATATACAACGATGGTGTCCCTGGATCTGTGAATT | 555 |
| Db | 481 | ATTCCACGAATGACACAGCCTATCTAATATACAACGATGGTGTCCCTGGATCTGTGAATT | 540 |
| Qy | 556 | ACA | 558 |

Db

541 ACA 543

Title: US-10-670-863-2 COPY 213 1274

RESULT 5

AF128888

| | | | | | |
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| LOCUS | AF128888 | 1654 bp | mRNA | linear | ROD 06-DEC-1999 |
|-------|----------|---------|------|--------|-----------------|

DEFINITION Mus musculus deoxyribonuclease DLAD mRNA, complete cds.

ACCESSION AF128888

VERSION AF128888.1 GI:6175549

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1654)

AUTHORS Shiokawa, D. and Tanuma, S.

TITLE DLAD, a novel mammalian divalent cation-independent endonuclease
with homology to DNase II

JOURNAL Nucleic Acids Res. 27 (20), 4083-4089 (1999)

MEDLINE 99428663

PUBMED 10497274

REFERENCE 2 (bases 1 to 1654)

AUTHORS Shiokawa, D. and Tanuma, S.

TITLE Direct Submission

JOURNAL Submitted (16-FEB-1999) Biochemistry, Science Univ. of Tokyo,
Shinjuku-ku Ichigaya Funagawara-machi 12, Tokyo 162-0826, Japan

| FEATURES | Location/Qualifiers |
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|----------|---------------------|

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            /strain="C57Bl/6"
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            /tissue type="liver"
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          /db_xref="GI:6175550"
          /translation="MTAKPLRTVLSLLFFALSGVLGTPEISCRNEYGEAVDWFIFYKL
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          LIYNDGVPGSVNYSRQYGHAKGLLVWNRQTQGFWLIIHVPKFPVPVHGVEYPTSGRRYQG
          TGICITFGYSQFEEIDFQLLVLPNIYSCFIPSTFHWKLIYMPRMCANSSSLKIPVRY
          LAELHSAQGLNLFVHFVFAKSSFYTDIDFTGWIAQKLKTHLLAQTWQKKKQELPSNCSLPY
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ORIGIN

Query Match 100.0%; Score 1062; DB 10; Length 1654;

Best Local Similarity 100.0%; Pred. No. 1.7e-307;

Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGACAGCAAAGCCTCTAAGAACAGTTCCTTCTTTGCTCTTCTTTGCCCTCTCTGGGGTC 60

Db 213 ATGACAGCAAAGCCTCTAAGAACAGTTCTTTCTTTGCTCTTCTTTGCCCTCTCTGGGGTC 272

[illegible]

Db 273 CTGGGGACACCAGAAATCTCATGCAGAAATGAATATGGTGAAGCTGTGGACTGGTTTATC 332

Qy 121 TTTTATAAGTTACCCAAAAGGACTAGCAAGGCAAGTGAAGAGGCGGGGCTGCAGTACCTG 180
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 333 TTTTATAAGTTACCCAAAAGGACTAGCAAGGCAAGTGAAGAGGCGGGGCTGCAGTACCTG 392

Qy 181 TACCTGGACTCCACAAGACAAACCTGGAACAAGAGCCTCTACCTGATTAACAGCACCAGG 240
|||||

Db 393 TACCTGGACTCCACAAGACAAACCTGGAACAAGAGCCTCTACCTGATTAACAGCACCAGG 452

Qy 241 AGTGCTCTGGGGAGGACCTTACAGCATCTGTATGACACACATAATTCCACGAATGACACA 300

Rattus.

REFERENCE 1 (bases 1 to 1498)

AUTHORS Tanuma,S. and Shiokawa,D.

TITLE Cloning of a cDNA encoding a rat DNase II-like acid DNase

JOURNAL Biochem. Biophys. Res. Commun. 265 (2), 395-399 (1999)

MEDLINE 20025354

PUBMED 10558878

REFERENCE 2 (bases 1 to 1498)

AUTHORS Shiokawa,D. and Tanuma,S.

TITLE Direct Submission

JOURNAL Submitted (19-AUG-1999) Biochemistry, Science University of Tokyo, Shinjuku-ku Ichigaya Funagawara-machi 12, Tokyo 162-0826, Japan

FEATURES

Location/Qualifiers

source 1..1498

/organism="Rattus norvegicus"

/mol_type="mRNA"

/strain="Wistar"

/db_xref="taxon:10116"

CDS 159..1229

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/protein_id="AAF13596.1"

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 PRRTSRGGTGMGLDYLYLDSTMRTWSKSHHLINSSRSSLGRTLEQLYEAHNAKNDTAY
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 AQSGLCITLKYSQYETIDSQLLVFQPNYISCFIPNIFRWELIHMPQMCAKSSASKIPS
 RRLTVLQSAQGLNFLHFAKSTFYTDDIFAAWIAQKLKVHLLVESWQRKNHELPSNCSL
 PYHVYNIKAIRGPLQSDFPSHHDHSKWCVSTKDSQARWTCIGDLNRSHPQALRSGGFI
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ORIGIN

Query Match 72.6%; Score 771.4; DB 10; Length 1498;

Best Local Similarity 83.4%; Pred. No. 3.9e-220;

Matches 890; Conservative 0; Mismatches 171; Indels 6; Gaps 1;

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|----|-----|---|-----|
| Qy | 1 | ATGACAGCAAAGCCTCTAAGAACAGTTCCTTTCTTTGCTCTTCTTTGCCCTCTCTGGGGTC | 60 |
| Db | 159 | ATGACAGCCCAGCCTCTAAAAGCAGCTCTTCCTTTGCTCTTCGTTGCCCTGTCCGGAGTC | 218 |
| Qy | 61 | CTGGGGACACCAGAAATCTCATGCAGAAATGAATATGGTGAAGCTGTGGACTGGTTTATC | 120 |
| Db | 219 | CTGGGGACACCAGTAATCTCGTGCATAAACGAAGATGGTAAAGCCGTGGACTGGTTTGCC | 278 |
| Qy | 121 | TTTTATAAGTTACCCAAAAGGACTAGCAAGGCAAGTGAAGAGGCGGGCTGCAGTACCTG | 180 |
| Db | 279 | TTTTATAAGTTACCCAGAAGGACCAGCAGAGGAGGTACAGGGATGGGGCTGGATTACCTG | 338 |
| Qy | 181 | TACCTGGACTCCACAAGACAAACCTGGAACAAGAGCCTCTACCTGATTAAACAGCACCAGG | 240 |
| Db | 339 | TACCTGGACTCCACAATGAGAACCTGGAGCAAGAGCCACCACCTGATTAAACAGCAGCAGG | 398 |
| Qy | 241 | AGTGCTCTGGGGAGGACCTTACAGCATCTGTATGACACACATAATTCCACGAATGACACA | 300 |
| Db | 399 | AGCTCCCTGGGAAGGACCCTGGAGCAGCTGTATGAAGCACACAATGCCAAGAATGACACA | 458 |
| Qy | 301 | GCCTATCTAATATACAACGATGGTGTCCCTGGATCTGTGAATTACAGCAGACAGTATGGA | 360 |
| Db | 459 | GCCTATCTGATATACAATGACGCTGTCCCTGCATCTGTGAATTACAGCGGAAATTACGGG | 518 |
| Qy | 361 | CATGCCAAAGGTCTGCTGGTATGGAACAGAACGAGGGGTTCTGGCTGATACACTCTGTT | 420 |
| Db | 519 | CATGCCAAAGGTCTGCTGGTATGGAACAGAGTGCAGGGGTTCTGGCTGATTCACTTCTATT | 578 |
| Qy | 421 | CCCAAGTTTCCCCCAGTTC-----ATGGCTATGAGTACCCAACCTCGGGGAGGCGATAT | 474 |
| Db | 579 | CCCAAGTTTCCCCCAGTTCGGGAAAAAGGCTATGAATACCCAAGCTCGGGGAGGCAATAT | 638 |

| | | | |
|----|-----|---|------|
| Qy | 1 | ATGACAGCAAAGCCTCTAAGAACAGTTCTTTCTTTGCTCTTCTTTGCCCCCTCTCTGGGGTTC | 60 |
| Db | 40 | ATGACAGCAAAGCCTCTAAGAACAGTTCTTTCTTTGCTCTTCTTTGCCCCCTCTCTGGGGTTC | 99 |
| Qy | 61 | CTGGGGACACCAGAAATCTCATGCAGAAATGAATATGGTGAAGCTGTGGACTGGTTTATC | 120 |
| Db | 100 | CTGGGGACACCAGAAATCTCATGCAGAAATGAATATGGTGAAGCTGTGGACTGGTTTATC | 159 |
| Qy | 121 | TTTTATAAGTTACCCAAAAGGACTAGCAAGGCAAGTGAAGAGGCGGGGCTGCAGTACCTG | 180 |
| Db | 160 | TTTTATAAGTTACCCAAAAGGACTAGCAAGGCAAGTGAAGAGGCGGGGCTGCAGTACCTG | 219 |
| Qy | 181 | TACCTGGACTCCACAAGACAAACCTGGAACAAGAGCCTCTACCTGATTAACAGCACCAGG | 240 |
| Db | 220 | TACCTGGACTCCACAAGACAAACCTGGAACAAGAGCCTCTACCTGATTAACAGCACCAGG | 279 |
| Qy | 241 | AGTGCTCTGGGGAGGACCTTACAGCATCTGTATGACACACATAATTCCACGAATGACACA | 300 |
| Db | 280 | AGTGCTCTGGGGAGGACCTTACAGCATCTGTATGACACACATAATTCCACGAATGACACA | 339 |
| Qy | 301 | GCCTATCTAATATACAACGATGGTGTCCCTGGATCTGTGAATTACAGCAGACAGTATGGA | 360 |
| Db | 340 | GCCTATCTAATATACAACGATGGTGTCCCTGGATCTGTGAATTACAGCAGACAGTATGGA | 399 |
| Qy | 361 | CATGCCAAAGGTCTGCTGGTATGGAACAGAACGCAGGGGTTCTGGCTGATACACTCTGTT | 420 |
| Db | 400 | CATGCCAAAGGTCTGCTGGTATGGAACAGAACGCAGGGGTTCTGGCTGATACACTCTGTT | 459 |
| Qy | 421 | CCCAAGTTTCCCCCAGTTCATGGCTATGAGTACCCAACCTCGGGGAGGCGATATGGACAA | 480 |
| Db | 460 | CCCAAGTTTCCCCCAGTTCATGGCTATGAGTACCCAACCTCGGGGAGGCGATATGGACAA | 519 |
| Qy | 481 | ACCGGCATCTGCATCACTTTCGGATACAGCCAGTTTGAGGAAAATAGATTTTTCAGCTCTTG | 540 |
| Db | 520 | ACCGGCATCTGCATCACTTTCGGATACAGCCAGTTTGAGGAAAATAGATTTTTCAGCTCTTG | 579 |
| Qy | 541 | GTCTTACAACCAAACATCTACAGCTGCTTCATTCCAAGCACCTTTCACTGGAAACTTATC | 600 |
| Db | 580 | GTCTTACAACCAAACATCTACAGCTGCTTCATTCCAAGCACCTTTCACTGGAAACTTATC | 639 |
| Qy | 601 | TACATGCCCCGGATGTGTGCCAACTCCAGTTCCTTAAAGATCCCTGTCCGGTACCTCGCT | 660 |
| Db | 640 | TACATGCCCCGGATGTGTGCCAACTCCAGTTCCTTAAAGATCCCTGTCCGGTACCTCGCT | 699 |
| Qy | 661 | GAACTGCACTCAGCCCAGGGTCTAAACTTCGTCCATTTTGCAAAATCAAGTTTTTATACT | 720 |
| Db | 700 | GAACTGCACTCAGCCCAGGGTCTAAACTTCGTCCATTTTGCAAAATCAAGTTTTTATACT | 759 |
| Qy | 721 | GATGACATCTTTACAGGATGGATAGCTCAAAAGTTGAAGACACATTTGTTAGCACAAACC | 780 |
| Db | 760 | GATGACATCTTTACAGGATGGATAGCTCAAAAGTTGAAGACACATTTGTTAGCACAAACC | 819 |
| Qy | 781 | TGGCAGAAAAAGAAACAAGAGCTTCCTTCAAACGTTCCTGCCTTACCATGTCTACAAC | 840 |
| Db | 820 | TGGCAGAAAAAGAAACAAGAGCTTCCTTCAAACGTTCCTGCCTTACCATGTCTACAAC | 879 |
| Qy | 841 | ATCAAGTCCATTGGGGTAACTTCCAAGTCTTACTTCAGTTCTCGCCAAGACCATTCACAA | 900 |
| Db | 880 | ATCAAGTCCATTGGGGTAACTTCCAAGTCTTACTTCAGTTCTCGCCAAGACCATTCACAA | 939 |
| Qy | 901 | TGGTGTGTTTCCATAAAGGGCTCCGCAAATCGCTGGACCTGCATTGGAGACCTAAATCGA | 960 |
| Db | 940 | TGGTGTGTTTCCATAAAGGGCTCCGCAAATCGCTGGACCTGCATTGGAGACCTAAATCGA | 999 |
| Qy | 961 | AGCCTACACCAAGCCTTAAGAGGTGGAGGATTATCTGTACAAAGAATCACTACATTTAC | 1020 |

Db 1000 AGCCTACACCAAGCCTTAAGAGGTGGAGGATTCATCTGTACAAAGAATCACTACATTTAC 1059
Qy 1021 CAGGCATTTTCATAAATTATATCTCCGTTATGGGTTCTGTAAG 1062
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Db 1060 CAGGCATTTTCATAAATTATATCTCCGTTATGGGTTCTGTAAG 1101

RESULT 2

US-09-949-434-1

; Sequence 1, Application US/09949434
; Patent No. 6767997
; GENERAL INFORMATION:
; APPLICANT: Eastman, Alan R.
; APPLICANT: Krieser, Ronald J.
; TITLE OF INVENTION: DEOXYRIBONUCLEASE II BETA PROTEINS AND cDNAS
; FILE REFERENCE: DC-0137
; CURRENT APPLICATION NUMBER: US/09/949,434
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/574,942
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1224
; TYPE: DNA
; ORGANISM: Mus sp.

US-09-949-434-1

Query Match 100.0%; Score 1062; DB 4; Length 1224;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy .1 ATGACAGCAAAGCCTCTAAGAACAGTTCCTTTCTTTGCTCTTCTTTGCCCTCTCTGGGGTC 60
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Db 40 ATGACAGCAAAGCCTCTAAGAACAGTTCCTTTCTTTGCTCTTCTTTGCCCTCTCTGGGGTC 99

Qy 61 CTGGGGACACCAGAAATCTCATGCAGAAATGAATATGGTGAAGCTGTGGACTGGTTTATC 120
|||||
Db 100 CTGGGGACACCAGAAATCTCATGCAGAAATGAATATGGTGAAGCTGTGGACTGGTTTATC 159

Qy 121 TTTTATAAGTTACCCAAAAGGACTAGCAAGGCAAGTGAAGAGGCGGGGCTGCAGTACCTG 180
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Db 160 TTTTATAAGTTACCCAAAAGGACTAGCAAGGCAAGTGAAGAGGCGGGGCTGCAGTACCTG 219

Qy 181 TACCTGGACTCCACAAGACAAACCTGGAACAAGAGCCTCTACCTGATTAACAGCACCAGG 240
|||||
Db 220 TACCTGGACTCCACAAGACAAACCTGGAACAAGAGCCTCTACCTGATTAACAGCACCAGG 279

Qy 241 AGTGCTCTGGGGAGGACCTTACAGCATCTGTATGACACACATAATTCCACGAATGACACA 300
|||||
Db 280 AGTGCTCTGGGGAGGACCTTACAGCATCTGTATGACACACATAATTCCACGAATGACACA 339

Qy 301 GCCTATCTAATATACAACGATGGTGTCCCTGGATCTGTGAATTACAGCAGACAGTATGGA 360
|||||
Db 340 GCCTATCTAATATACAACGATGGTGTCCCTGGATCTGTGAATTACAGCAGACAGTATGGA 399

Qy 361 CATGCCAAAGGTCTGCTGGTATGGAACAGAACGCAGGGGTTCTGGCTGATACACTCTGTT 420
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Db 400 CATGCCAAAGGTCTGCTGGTATGGAACAGAACGCAGGGGTTCTGGCTGATACACTCTGTT 459

Qy 421 CCCAAGTTTCCCCAGTTTCATGGCTATGAGTACCCAACCTCGGGGAGGCGATATGGACAA 480
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Db 460 CCCAAGTTTCCCCAGTTTCATGGCTATGAGTACCCAACCTCGGGGAGGCGATATGGACAA 519

Qy 481 ACCGGCATCTGCATCACTTTTCGGATACAGCCAGTTTGAGGAAATAGATTTTTCAGCTCTTG 540
|||||
Db 520 ACCGGCATCTGCATCACTTTTCGGATACAGCCAGTTTGAGGAAATAGATTTTTCAGCTCTTG 579

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| Qy | 541 | GTCTTACAACCAAACATCTACAGCTGCTTCATTCCAAGCACCTTTCACTGGAAACTTATC | 600 |
| | | | |
| Db | 580 | GTCTTACAACCAAACATCTACAGCTGCTTCATTCCAAGCACCTTTCACTGGAAACTTATC | 639 |
| Qy | 601 | TACATGCCCCGGATGTGTGCCAACTCCAGTTCCTTAAAGATCCCTGTCCGGTACCTCGCT | 660 |
| | | | |
| Db | 640 | TACATGCCCCGGATGTGTGCCAACTCCAGTTCCTTAAAGATCCCTGTCCGGTACCTCGCT | 699 |
| Qy | 661 | GAAGTGCCTCAGCCCAGGGTCTAAACTTCGTCCATTTTGCAAAATCAAGTTTTTATACT | 720 |
| | | | |
| Db | 700 | GAAGTGCCTCAGCCCAGGGTCTAAACTTCGTCCATTTTGCAAAATCAAGTTTTTATACT | 759 |
| Qy | 721 | GATGACATCTTTACAGGATGGATAGCTCAAAAGTTGAAGACACATTTGTTAGCACAAC | 780 |
| | | | |
| Db | 760 | GATGACATCTTTACAGGATGGATAGCTCAAAAGTTGAAGACACATTTGTTAGCACAAC | 819 |
| Qy | 781 | TGGCAGAAAAAGAAACAAGAGCTTCCTTCAAAGTTCCTTCCCTGCCTTACCATGTCTACAAC | 840 |
| | | | |
| Db | 820 | TGGCAGAAAAAGAAACAAGAGCTTCCTTCAAAGTTCCTTCCCTGCCTTACCATGTCTACAAC | 879 |
| Qy | 841 | ATCAAGTCCATTGGGGTAACTTCCAAGTCTTACTTCAGTTCTCGCCAAGACCATTCCAAA | 900 |
| | | | |
| Db | 880 | ATCAAGTCCATTGGGGTAACTTCCAAGTCTTACTTCAGTTCTCGCCAAGACCATTCCAAA | 939 |
| Qy | 901 | TGGTGTGTTTCCATAAAGGGCTCCGCAAATCGCTGGACCTGCATTGGAGACCTAAATCGA | 960 |
| | | | |
| Db | 940 | TGGTGTGTTTCCATAAAGGGCTCCGCAAATCGCTGGACCTGCATTGGAGACCTAAATCGA | 999 |
| Qy | 961 | AGCCTACACCAAGCCTTAAGAGGTGGAGGATTCATCTGTACAAAGAATCACTACATTTAC | 1020 |
| | | | |
| Db | 1000 | AGCCTACACCAAGCCTTAAGAGGTGGAGGATTCATCTGTACAAAGAATCACTACATTTAC | 1059 |
| Qy | 1021 | CAGGCATTTTCATAAATTATATCTCCGTTATGGGTTCTGTAAG | 1062 |
| | | | |
| Db | 1060 | CAGGCATTTTCATAAATTATATCTCCGTTATGGGTTCTGTAAG | 1101 |

| | | | |
|----|------|---|------|
| Db | 465 | CTGATATACAATGACGCTGTCCCTGCATCTGTGAATTACAGCGGAAATTACGGGCATGCC | 524 |
| Qy | 301 | AAAGGTCTGCTGGTATGGAACAGAACGCAGGGGTTCTGGCTGATACACTCTGTTCCCAAG | 360 |
| Db | 525 | AAAGGTCTGCTGGTATGGAACAGAGTGCAGGGGTTCTGGCTGATTCACTTCTATTCCCAAG | 584 |
| Qy | 361 | TTTCCCCCAGTTC-----ATGGCTATGAGTACCCAACTCGGGGAGGCGATATGGACAA | 414 |
| Db | 585 | TTTCCCCCAGTTCGGGAAAAGGCTATGAATACCCAAAGCTCGGGGAGGCAATATGCACAA | 644 |
| Qy | 415 | ACCGGCATCTGCATCACTTTCCGATACAGCCAGTTTGAGGAAATAGATTTTCAGCTCTTG | 474 |
| Db | 645 | AGTGGCCTCTGCATCACTCTCAAATACAGCCAGTATGAGACAATAGATTCTCAGCTCTTG | 704 |
| Qy | 475 | GTCTTACAACCAACATCTACAGCTGCTTCATTCCAAGCACCTTTCACTGGAAACTTATC | 534 |
| Db | 705 | GTCTTCCAGCCAAACATCTACAGCTGTTTCATCCCAAACATCTTTCGCTGGGAACTCATC | 764 |
| Qy | 535 | TACATGCCCCGGATGTGTGCCAACTCCAGTTCCTTAAAGATCCCTGTCCGGTACCTCGCT | 594 |
| Db | 765 | CACATGCCTCAGATGTGTGCCAAGTCCAGTGCCTCAAAGATCCCTAGCCGGCGCTCACT | 824 |
| Qy | 595 | GAACTGCACTCAGCCCAGGGTCTAAACTTCGTCCATTTTGCAAATCAAGTTTTTATACT | 654 |
| Db | 825 | GTACTTCAGTCAGCCCAGGGTCTAAACTTCCTCCATTTTGCGAAATCAACTTTTTATACT | 884 |
| Qy | 655 | GATGACATCTTTACAGGATGGATAGCTCAAAAGTTGAAGACACATTTGTTAGCACAAACC | 714 |
| Db | 885 | GATGACATCTTTGCAGCCTGGATAGCTCAAAAGCTGAAGGTGCATTTGCTGGTAGAATCC | 944 |
| Qy | 715 | TGGCAGAAAAAGAAACAAGAGCTTCCTTCAAACGTTCCTGCCTTACCATGTCTACAAC | 774 |
| Db | 945 | TGGCAGCGAAAGAACCACGAGCTTCCTTCAAACGTTCCTGCCTTACCATGTCTACAAC | 1004 |
| Qy | 775 | ATCAAGTCCATTGGGGTAACTTCCAAGTCTTACTTCAGTTCTCGCCAAGACCATTCCAAA | 834 |
| Db | 1005 | ATCAAGGCCATTTCGGGGACCTCTGCAGTCCGACTTCCTTCTCATCAGACCATTCCAAA | 1064 |
| Qy | 835 | TGGTGTGTTTCCATAAAGGGCTCCGCAAATCGCTGGACCTGCATTGGAGACCTAAATCGA | 894 |
| Db | 1065 | TGGTGTGTTTCCACAAAGGACTCTCAGGCTCGCTGGACCTGTATTGGAGACCTAAATCGG | 1124 |
| Qy | 895 | AGCCTACACCAAGCCTTAAGAGGTGGAGGATTCACTGTACAAAGAATCACTACATTTAC | 954 |
| Db | 1125 | AGCCACATCAAGCCTTGAGAAGTGGAGGATTTATCTGTTTGAAGAATCGGTACATTTAC | 1184 |
| Qy | 955 | CAGGCATTTCATAAATTATATCTCCGTTATGGGTTCTGTAA | 995 |
| Db | 1185 | CAGTCATTTGATAGGTTAGTTTCCCATTAATGCCTCCTGTAA | 1225 |